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Qy 1270 E-TDSCSRSHRDQGVGLGLHAKELCEVDEQDSVL--QVTRRLPILPILLTLEV 1326
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Qy 1372 SVTQSLTNGTAQTPSASRKSLSAPSW--PGVRLGSLM--EQLLKTLR-----YNFLP 1421
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Qy 1422 EALD-----PVGU-----HQERTLOCLNVRVTVOSLACLEADHTVGFILQSLNFK 1469
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Qy 1470 WHFHLPOLARDIO--VNIG---YLCOACTSLHRSRMLQHYLQKNGDGLPSAVA--QRV 1522
Db 1366 HSDKGLPLRDONGIUVLLGERAAKCRVAKALHYKEL--EPQKGTFAILESLSINNK 1423
Qy 1523 QRPPSAAASAPSSSKQ--PAADTEASEQQALH 1552
Db 1424 QPEASAGVLEVMKHFGELEIQTWYKHL 1454

RESULT 5

US-08-471-112A-3
; Sequence 3, Application US/08471112A
; Patent No. 6313264
; GENERAL INFORMATION:
; APPLICANT: Molnar-Kimbar, Katherine L.
; APPLICANT: Failli, Amedeo P.
; APPLICANT: Caggiano, Thomas J.
; APPLICANT: Nakanishi, Koji
; APPLICANT: Chen, Yanqiu
; TITLE OF INVENTION, SPECTATOR PROTEINS OF RAPAMYCIN
; NUMBER OF SEQUENCES, 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,112A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/384,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/312,023

; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,975
; FILING DATE: 08-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Siekman, Michael T.
; REGISTRATION NUMBER: 36,276
; REFERENCE/DOCKET NUMBER: 01142.0058-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2549 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-112A-3

Query Match 1.6%, Score 144.5, DB 3, Length 2549;
Best Local Similarity 18.6%, Pred. No. 0.0017,
Matches 336; Conservative 238; Mismatches 628; Indels 605; Gaps 87;

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Qy 285 SLHKCALDDRRRLHQPADQGLI-----QQMDCLALTPGDIPHPAPVLLAWALLRHTLNP 340
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Qy 341 ETSSVVVKIG-----CTA----- 353
Db 326 QSNALVGLLGYSSHQGLMGFTSPSPAKSTLVSRCCRDLMBEKPOQVQWVKRNSEN 385
Qy 354 --IQNLVPOYLTRL-----LQSLASGNDCTTS-----TACHVCYVGLLSPVLT 394
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Qy 439 ---SVCGMPHLLSPQLLQALVSGHSTAKVYSLDKMSFYNELYKPKHVDVSHEDG 495
Db 506 EPMKLVGLSPALTAVLDLSHQIPQLK---KDIDGLLKH--LSLVLPKHP----- 551
Qy 496 TLWRKQTPK-LIYPLGGQTNLRIPQGT-VQVMDLDRAYLVVRWVYSYSMTLP----- 546
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Qy 547 -----TCB---IEMLLHVSTADVIQCRVKPTIDLVHKVI-----STD 584
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Qy 585 STADCLLPITSRYML-----LORLTTVISPPDVVIAVCNCLTV--LAARNA----- 631
Db 670 DIRYCVLASLDERFDAHLAQENLQALFVALNDQVFEIRELAIC-TVGRSLSMNPAFVMP 728
Qy 632 -----KVTDLRHTGF-----LPFAHPVSSLSOMISABGMNAGYGN-----L 670
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Qy 671 LKNSQPGQEGYGTIAFLRLITTLVKQLGSTQSGLVFCVMPVLEKMLPSYHKRYNSH 730
Db 782 KLDKDPDPNPGVINNVLATI-----GEL---AQVSGI-----EM----- 816
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OM protein - protein search, using aw model

Run on: December 30, 2004, 15:14:08 / Search time 215.263 Seconds
(without alignments)
2329.449 Million cell updates/sec

Title: US-10-719-385-2

Perfect score: 9007

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Gapop 10.0 / Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	9003	100.0	1753	17	US-10-719-385-15
9	9002	99.9	1753	17	US-10-719-385-6
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11	9001	99.9	1753	17	US-10-719-385-16
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15	8997	99.9	1753	17	US-10-719-385-9	Sequence 9, Appli
16	8991	99.8	1753	17	US-10-719-385-17	Sequence 17, Appli
17	8991	99.8	1753	17	US-10-719-385-19	Sequence 19, Appli
18	8985.5	99.8	1752	17	US-10-719-385-5	Sequence 5, Appli
19	8939	99.2	1745	17	US-10-719-385-21	Sequence 21, Appli
20	8939	99.2	1745	17	US-10-719-385-22	Sequence 22, Appli
21	8927	99.1	1745	17	US-10-719-385-23	Sequence 23, Appli
22	5270	58.5	1111	17	US-10-719-385-24	Sequence 24, Appli
23	4093	45.4	953	17	US-10-719-385-25	Sequence 25, Appli
24	2420	26.9	526	17	US-10-719-385-26	Sequence 26, Appli
25	369.5	4.1	2026	16	US-10-437-963-135530	Sequence 135530, Ap
26	305	3.4	63	14	US-10-106-698-5917	Sequence 5917, Ap
27	245	2.7	1745	16	US-10-437-963-173637	Sequence 173637, Ap
28	176.5	2.0	2905	16	US-10-437-963-154118	Sequence 154118, Ap
29	175.5	1.9	1676	14	US-10-128-714-8246	Sequence 8246, Ap
30	169.5	1.9	2621	16	US-10-437-963-122168	Sequence 122168, Ap
31	166	1.8	2122	16	US-10-437-963-189782	Sequence 189782, Ap
32	165	1.8	1545	14	US-10-128-714-3246	Sequence 3246, Ap
33	160.5	1.8	2462	16	US-10-437-963-114113	Sequence 114113, Ap
34	157	1.7	3859	16	US-10-408-765A-354	Sequence 354, App
35	156	1.7	2827	15	US-10-424-599-256710	Sequence 256710, Ap
36	155	1.7	1357	14	US-10-369-493-2224	Sequence 2224, Ap
37	155	1.7	2834	15	US-10-424-599-256711	Sequence 256711, Ap
38	153	1.7	3830	17	US-10-723-860-2568	Sequence 2568, Ap
39	152.5	1.7	2159	16	US-10-437-963-108860	Sequence 108860, Ap
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41	151	1.7	3225	16	US-10-408-765A-214	Sequence 254, App
42	151	1.7	4464	14	US-10-369-493-5019	Sequence 5019, Ap
43	148.5	1.6	2811	17	US-10-810-352-39	Sequence 39, Appli
44	148	1.6	2593	16	US-10-437-963-114115	Sequence 114115, Ap
45	147.5	1.6	2209	9	US-09-903-941-1903	Sequence 1903, Ap
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52	147.5	1.6	2859	13	US-10-087-192-249	Sequence 249, App
53	147	1.6	3907	14	US-10-171-311-2	Sequence 2, Appli
54	147	1.6	3925	14	US-10-171-311-6	Sequence 6, Appli
55	145.5	1.6	2848	14	US-10-369-493-6048	Sequence 6048, Ap
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59	144	1.6	2405	16	US-10-437-963-106815	Sequence 106815, Ap
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61	143	1.6	1783	15	US-10-188-832-86	Sequence 86, Appli
62	143	1.6	2549	16	US-10-701-490-2	Sequence 2, Appli
63	143	1.6	3899	14	US-10-171-311-4	Sequence 4, Appli
64	143	1.6	3917	14	US-10-171-311-8	Sequence 8, Appli
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70	140	1.6	1867	16	US-10-437-963-137806	Sequence 137806, Ap
71	140	1.6	3878	14	US-10-080-608A-11	Sequence 11, Appli
72	140	1.6	3911	14	US-10-370-685-100	Sequence 100, App
73	140	1.6	3911	16	US-10-408-765A-1839	Sequence 1839, Ap
74	139.5	1.5	4096	17	US-10-473-127-571	Sequence 571, App
75	139.5	1.5	4097	15	US-10-363-616-415	Sequence 415, App
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78	139.5	1.5	4128	15	US-10-363-616-416	Sequence 416, App
79	139.5	1.5	4128	17	US-10-473-127-574	Sequence 574, App
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84	138	1.5	1479	16	US-10-437-963-106122	Sequence 106122, Ap
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86	136.5	1.5	4128	17	US-10-473-127-573	Sequence 573, App